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Application Number		09391861
Filing Date		1999-09-07
First Named Inventor	Arlen R. Thomason	
Art Unit	1633	
Examiner Name	Fereydown G. Sajjadi	
Attorney Docket Number	99-371	

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↓	3	0088046	EP		1983-09-07	Ciba Geigy AG		<input type="checkbox"/>

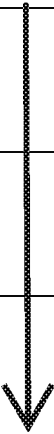
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/F.S./	4	0143949	EP		1985-06-12	Terumo Corp.		<input type="checkbox"/>
	5	0154316	EP		1985-09-11	Takeda Chemical Industries Ltd.		<input type="checkbox"/>
	6	0505500	EP		1992-09-30	Applied Research Systems et al.		<input type="checkbox"/>
	7	91/09955	WO		1991-07-11	Applied Research Systems et al.		<input type="checkbox"/>
	8	91/10425	WO		1991-07-25	Brown University Research Foundation		<input type="checkbox"/>
	9	91/10470	WO		1991-07-25	Brown University Research Foundation		<input type="checkbox"/>
	10	93/15722	WO		1993-08-19	Syntex Inc.		<input type="checkbox"/>
	11	94/20069	WO		1994-09-15	Amgen Inc.		<input type="checkbox"/>
	12	94/28122	WO		1994-12-08	Ontario Cancer Institute		<input type="checkbox"/>
	13	95/05452	WO		1995-02-23	Cyotherapeutics, Inc.		<input type="checkbox"/>
	14	95/34670	WO		1995-12-21	Children's Hospital, Inc.		<input type="checkbox"/>


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/F.S./	15	96/37609	WO		1996-11-28	Zeneca Ltd.		<input type="checkbox"/>
	16	96/40958	WO		1996-12-19	Baylor College of Medicine		<input type="checkbox"/>
	17	96/41865	WO		1996-12-27	Ariad Gene Therapeutics, Inc.		<input type="checkbox"/>
	18	97/31899	WO		1997-09-04	Ariad Gene Therapeutics, Inc.		<input type="checkbox"/>

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/F.S./	1	BISHOP, "Chromosomal insertion of foreign DNA," Reprod. Nutr. Dev. 36(6):607-18 (1996)	<input type="checkbox"/>
	2	BORK et al., "Go hunting in sequence databases but watch out for the traps," Trends Genet. 12(10):425-27 (1996)	<input type="checkbox"/>
	3	BORK et al., "Predicting functions from protein sequences -- where are the bottlenecks?" Nature Genetics 18 (4):313-18 (1998)	<input type="checkbox"/>
	4	BORK, "Powers and pitfalls in sequence analysis: the 70% hurdle," Genome Res. 10(4):398-400 (2000)	<input type="checkbox"/>
	5	BRENNER, "Errors in genome annotation," Trends Genet. 15(4):132-33 (1999)	<input type="checkbox"/>

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/F.S./	6	DOERKS et al., "Protein annotation: detective work for function prediction," Trends Genet. 14(6):248-50 (1998)	<input type="checkbox"/>
	7	MIKKELSEN, " Interpreting sequence motifs: a cautionary note," Trends Genet. 9(5):159 (1993)	<input type="checkbox"/>
	8	NAKAMURA et al., "The murine lymphotoxin-beta receptor cDNA: isolation by the signal sequence trap and chromosomal mapping," Genomics 30(2):312-19 (1995)	<input type="checkbox"/>
	9	NGO et al., The Protein Folding Problem and Tertiary Structure Prediction 492-95 (Birkhauser, Boston MA) (1994)	<input type="checkbox"/>
	10	NIYOGI, "The influence of chain length and base composition on the specific association of oligoribonucleotides with denatured deoxyribonucleic acid," J. Biol. Chem. 244(6):1576-81 (1969)	<input type="checkbox"/>
	11	POLEJAEVA et al., "New advances in somatic cell nuclear transfer: application in transgenesis," Theriogenology 53 (1):117-26 (2000)	<input type="checkbox"/>
	12	RULICKE et al., "Germ line transformation of mammals by pronuclear microinjection," Exp. Physiol. 85(6):589-601 (2000)	<input type="checkbox"/>
	13	SKOLNICK et al., "From genes to protein structure and function: novel applications of computational approaches in the genomic era," Trends Biotechnol. 18(1):34-39 (2000)	<input type="checkbox"/>
	14	SMITH et al., "The challenges of genome sequence annotation or "the devil is in the details," Nat. Biotechnol. 15 (12):1222-23 (1997)	<input type="checkbox"/>

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